Kevin Doyle

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Evolutionary biologist with a strong passion for statistical data analysis and computational genomic research.

Education:

MA Biology - Applied Evolution

Stony Brook University, Stony Brook, NY   2015
Relevant coursework: Biometry, Computational Biology, Population Genetics
GPA: 3.8

BS Biology - Ecology & Evolution

Stony Brook University, Stony Brook, NY   2013
Minor: Ecosystems and Human Impact

Qualifications:

- Unix Systems
- R
- Python
- HTML

- Algorithm Design
- Git / GitHub
- Genomic Data Analysis
- MS Office (Word, Excel)

- Software Compilation
- NGS Analysis
- Debugging / Troubleshooting
- Wet Laboratory Skills

Related Experience:

Hollister Lab of Evolutionary Genomics

Stony Brook University, Stony Brook, NY   Aug 2015 - May 2016
Project: Evolution of allopolyploidy in *Arabidopsis thaliana*
Utilized Genome Analysis Toolkit (GATK) best practices pipeline to acquire, organize, and analyzed Illumina next-generation sequencing (NGS) data from the National Center for Biotechnology Information (NCBI) Sequence Read Archive (SRA) database. Analyzed haplotype variance to infer global patterns of genomic divergence. Tools used were SRA Toolkit, SamTools, Picard Tools, Stampy, GATK, UnifiedGenotyper, HaplotypeCaller, VCFtools, SnpEff.
- Created scripts to enhance existing pipelines to streamline analyses
- Maintained data and documentation organized on Unix server
- Utilized GATK, Biopython, & R to analyze variation among individuals

Computational Biology Coursework

Stony Brook University, Stony Brook, NY   Aug 2015 - Dec 2015
Created Python scripts to coincided with lectures pertaining to topics such as sequence alignment (pairwise & multiple), genome assembly, and gene finding using Hidden Markov Models. Course project involved creating functioning code from minimally existing Python code to perform an analysis on the accuracy of the duplication-mutation with complementarity (DMC) algorithm specified in *Navlakha & Kingsford 2011* on generating phylogenetic trees using a combination of protein-protein interaction (PPI) networks and genomic data.

Biometry Coursework

Stony Brook University, Stony Brook, NY   Jan 2015 - May 2015

Rigorously utilized R to perform a wide variety of statistical analyses including linear/nonlinear regression, correlation, generalized linear models, probability distributions, maximum likelihood estimates, hypothesis testing, multiple comparisons analysis, bootstrapping and jackknifeing, data visualization with ggplot, ANOVA/ANCOVA, model selection/comparison, and principal component analysis.

Baines Lab of Aquatic Ecology

Stony Brook University, Stony Brook, NY   Aug 2013 - May 2016

Project: Fe Limitation in the Copepod *Acartia tonsa*

Designed an experiment to determine the critical Fe:C threshold where iron limitation occurs in *Acartia tonsa* and performed statistical analyses using R and Excel to find where threshold occurred. Scrupulously clean conditions had to be maintained regarding all reagents and surfaces to prevent trace metal contamination.

- Maintained organized records of calculations and analyses
- Used R package 'segmented' to estimate where Fe threshold occurred by calculating the breakpoint between two separate linear regressions of egg production with replete Fe and egg production with deplete Fe
- Produced figures with R and Excel
- Grew cell and zooplankton cultures
- Created various chemical reagents to use in experiment
- Wrote paper (*Estimating the Threshold of Iron Limitation in the Copepod Acartia tonsa*) for publication

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Other Experience:

Department of Environmental Conservation, Field Technician

Ridge, NY 11961   May 2016 - September 2016 (Seasonal)

Surveyed historic breeding sites across Long Island to determine the status of tiger salamander (*Ambystoma tigrinum*) and diamondback terrapins (*Malaclemys terrapin*) populations and their respective habitats. Also Assisted in setting up exclosures on piping plover (*Charadrius melodus*) breeding sites.

- Performed atmospheric and water chemistry analyses
- Surveyed ponds for *A. tigrinum* using dip net and seine
- Used ArcMap data in Google Earth to locate sites and entered data using Excel

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Other Training:

Rosalind & Codecademy Exercises

http://rosalind.info, http://codecademy.com   May 2016 - Current

Using Python to complete problems under Rosalind's bioinformatics stronghold category and completing Codecademy course on SQL. Some topics completed thus far are:

- Counting nucleotides and SNPs
- Transcribing and translating DNA
- Calculating probability of inherited alleles
- Dynamic programming
- Finding DNA motifs